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Research Article

Two new species of *Fulvifomes* (Hymenochaetales, Basidiomycota) from South America

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Abstract

Two new species of *Fulvifomes* are described from specimens collected in South America (Ecuador and Bolivia) based on morphological and molecular evidence. The species *Fulvifomes bolivianus* is characterized by perennial, pileate, solitary basidiocarp; ungulate pilei; olivaceous, encrusted, rough, concentrically sulcate, irregularly cracked pileal surface; umber and glossy pore surface; circular pores measuring 7–8 per mm; thick and entire dissepiments; a dimitic hyphal system; and subglobose basidiospores measuring 4.7–5.4 × 4–4.5 µm. *Fulvifomes fragilis* is characterized by annual, pileate, imbricate basidiocarps; curry yellow to yellowish brown pileal surface; yellowish brown and narrow pileal margin; yellow and rugged pore surface; circular to elliptical pores measuring 5–6 per mm; thick and entire dissepiments; a dimitic hyphal system; and broadly ellipsoid basidiospores measuring 3.9–5.1 × 3–3.7 µm. Phylogenetically, the two new species formed two distinct lineages in the *Fulvifomes* clade based on internal transcribed spacer (ITS) and nuclear-encoded large subunit rRNA gene (nLSU) sequences. The differences between the new species and morphologically similar and phylogenetically related species are also discussed.

Key words: Hymenochaetales, phylogenetic analysis, taxonomy, wood-decaying fungi

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Introduction

Hymenochaetaceae is an important family of wood-inhabiting fungi. Species diversity and taxonomy of the family have been systematically studied, and around 920 species have been recognized in the family (Dai 2010; Wu et al. 2022; Dong et al. 2024; Liu et al. 2025). Some very important medicinal fungi belong to this family (Chu et al. 2023; Lv et al. 2023; Yang et al. 2023; Lang et al. 2024; Ma et al. 2024; Zhang et al. 2024). *Fulvifomes* Murrill is a genus belonging to Hymenochaetaceae, and it was described based on *F. robiniae* (Murrill) Murrill, grouping species of polypores with perennial basidiocarps, brown and woody context, and colored basidiospores (Murrill 1903; Murrill 1914). The genus was treated as a synonym of *Phellinus* Quél. for several decades (Gilbertson and Ryvarden 1986; Larsen and Cobb-Poulle 1990) until Wagner and Fischer (2002) confirmed *Fulvifomes* as an independent genus

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based on nuclear-encoded large subunit rRNA gene (nLSU) sequences. Due to uniform morphology, traditional *Fulvifomes* classification only enables definition of a limited number of species based on a few distinct features (Dai 2010; Hattori et al. 2014; Salvador-Montoya et al. 2018; Wu et al. 2022). Based on molecular and morphological analyses, Zhou (2014) revised the definition of *Fulvifomes*. The genus is characterized by basidiomata that are annual to perennial, pileate or substipitate, effused-reflexed or substipitate with a contracted base, solitary or imbricate, and corky to woody hard; pileal surface tomentose or glabrous, with or without a crust; context homogenous or duplex; hyphal system monomitic or dimitic; generative hyphae simple septate; setal elements absent; basidiospores subglobose to ellipsoid, yellowish to brown, fairly thick- to thick-walled, smooth; causing a white rot (Zhou 2014; Zhou 2015; Wu et al. 2022). Most species of *Fulvifomes* grow on dead angiosperm trees or wood, although a few can inhabit living trees (Ji et al. 2017; Wu et al. 2022). Most species of the genus have been found in tropical or subtropical areas of Asia, America, and Africa (Ediriweera et al. 2014; Olou et al. 2019; Fatima et al. 2023; Zhou et al. 2023; Zhao et al. 2024).

Moreover, many species of *Fulvifomes* are forest pathogens, and some species have therapeutic properties (Dai et al. 2007; Wu et al. 2019; Yuan et al. 2023). Three previously undescribed limonoids (fulvifomins A–C) were isolated from *Fulvifomes xylocarpicola* T. Hatt., Sakay. & E.B.G. Jones, of which fulvifomin B exhibited antimalarial and antitubercular activities (Isaka et al. 2021). To date, more than 50 species have been recorded in *Fulvifomes* (Wu et al. 2022), but there have been only a few reports on the isolation of bioactive compounds from *Fulvifomes* species (Ding et al. 2019; Isaka et al. 2021; Lin et al. 2024). One contributing factor may be the relatively recent recognition of *Fulvifomes* as an independent genus. Presently, *Fulvifomes* is widely accepted as an independent genus in Hymenochaetaceae, and several new taxa of the genus have been detected based on molecular and morphological evidence (Martínez et al. 2023; Zhou et al. 2023; Suh et al. 2024).

During an investigation on the wood-inhabiting fungi from South America (Ecuador and Bolivia), samples were collected with morphological characteristics fitting *Fulvifomes*. Phylogenetically, they formed independent lineages within *Fulvifomes*. Therefore, we describe two new species of *Fulvifomes* in the present paper.

Materials and methods

Morphological studies

The studied specimens are deposited in the Fungarium of the Institute of Microbiology, Beijing Forestry University (BJFC), Beijing, China. Morphological descriptions were based on field notes and voucher specimens. The microscopic analysis follows Wu et al. (2022), and the special color terms follow Anonymous (1969) and Petersen (1996). Microscopic features, measurements, and illustrations were made from slide preparations stained with Melzer's reagent (IKI) and Cotton Blue (CB). The sections were studied at magnifications up to ×1,000 using a Nikon Eclipse 80i microscope with phase contrast illumination. The following abbreviations are used:

KOH = 5% potassium hydroxide, **IKI** = Melzer's reagent, **IKI[+]** = dextrinoid, **IKI–** = both inamyloid and non-dextrinoid, **CB** = Cotton Blue, **CB+** = cyanophilous, **CB–** = weakly acyanophilous; **L** = arithmetic average of spore length, **W** = arithmetic average of spore width, **Q** = L/W ratios, and **n** = number of basidiospores measured from a given number of specimens. Basidiospores were measured from sections cut from the tubes.

DNA extraction, amplification, and sequencing

The CTAB rapid plant genome extraction kit-DN14 (Aidlab Biotechnologies Co., Ltd., Beijing) was used to obtain DNA from dried specimens. The primer pair ITS4 and ITS5 was used for amplification of the ITS region, while the primer pair LR0R and LR7 was used to amplify the nuclear large subunit ribosomal RNA gene (nLSU) (White et al. 1990). The PCR procedure for ITS was as follows: initial denaturation at 95 °C for 3 min, followed by 35 cycles at 94 °C for 40 s, 54 °C for 45 s, and 72 °C for 1 min, and a final extension at 72 °C for 10 min. The PCR procedure for nLSU was as follows: initial denaturation at 94 °C for 1 min, followed by 35 cycles at 94 °C for 30 s, 50 °C for 1 min, and 72 °C for 1.5 min, and a final extension at 72 °C for 10 min. The PCR products were purified and sequenced at the Beijing Genomics Institute, China, with the same primers. Reference ITS and nLSU sequences of *Fulvifomes* were downloaded from GenBank according to Wu et al. (2022) and Suh et al. (2024). All sequences analyzed in this study are listed in Table 1. Both ITS and nLSU datasets were aligned using MAFFT v. 7 (Katoh and Standley 2013) under the G-INS-i option and manually proofread in BioEdit (Hall 1999). Alignments were subsequently spliced and transformed into formats in Mesquite v. 3.2 (Maddison and Maddison 2017).

Phylogenetic analyses

Phylogenetic analyses were performed using maximum likelihood (ML) and Bayesian inference (BI) methods based on ITS + nLSU datasets. Sequence alignments were deposited in TreeBase (http://purl.org/phylo/treebase; submission ID: 32179; reviewer access URL: http://purl.org/phylo/treebase/phylows/study/TB2:S32179?x-access-code=5f27f003f433eeb85630b37affbf34ef&format=html). *Phellinus betulinus* (Murrill) Parmasto and *P. populicola* Niemelä were used as outgroups in the phylogeny of *Fulvifomes* (Wu et al. 2022). The best-fit evolutionary model was estimated using jModelTest under Akaike Information Criterion (Guindon and Gascuel 2003; Posada 2008). The ML method was performed using RAxML-HPC2 through the CIPRES Science Gateway (Miller et al. 2010), and branch support (BS) was determined by 1000 bootstrap replicates. The BI method was conducted with MrBayes v. 3.2.6 (Ronquist et al. 2012). Four chains were run for 2 million generations (split deviation frequency value was less than 0.01), and trees were sampled every 100 generations. The first 25% of trees were removed, and the remaining ones were used to construct a 50% majority-rule consensus tree and to calculate Bayesian Posterior Probabilities (BPPs). Phylogenetic trees were visualized using FigTree v. 1.4.3. Branches that received bootstrap support for ML (≥ 75% BS) and BPPs (≥ 0.95 BPPs) were considered to be significantly supported.

Table 1. Information for the sequences used in this study.

Species name	Sample no.	Location	GenBank accessions no.		References
			ITS	nLSU	
Flaviporellus splitgerberi	JV 1908/6	French Guiana	MZ484525	MZ437386	Wu et al. (2022)
Fomitiporella caryophylli	CBS 448.76	India	AY558611	AY059021	Jin et al. (2005)
Fulvifomes acaciae	JV 0312/23.4-J	USA	OP828594	OP828596	Zhou et al. (2023)
Fulvifomes acaciae	JV 2203/71	Costa Rica	OP828595	OP828596	Zhou et al. (2023)
Fulvifomes azonatus	Cui 8452	China	MH390417	MH390396	Wu et al. (2022)
Fulvifomes azonatus	Dai 17470	China	MH390418	MH390395	Wu et al. (2022)
Fulvifomes bolivianus	**JV 2311/6-J**	**Bolivia**	**PV749018**	–	**Present study**
Fulvifomes bolivianus	**JV 2411/15J**	**Bolivia**	**PV749017**	–	**Present study**
Fulvifomes boninensis	FFPRI 421009	Japan	LC315786	LC315777	Hattori et al. (2022)
Fulvifomes caligoporus	Dai 17668	China	MH390420	MH390390	Wu et al. (2022)
Fulvifomes caligoporus	Dai 17660	China	MH390421	MH390391	Wu et al. (2022)
Fulvifomes centroamericanus	JV 0611/III	Guatemala	KX960763	KX960764	Ji et al. (2017)
Fulvifomes centroamericanus	JV 0611/8P	USA	KX960757	–	Ji et al. (2017)
Fulvifomes coffeatoporus	JV0904_1	USA	KX960762	KX960765	Wu et al. (2022)
Fulvifomes coffeatoporus	JV0312_24.10J	USA	KX960760	KX960766	Wu et al. (2022)
Fulvifomes coffeatoporus	JV1008_21	USA	KX960761	KX960767	Wu et al. (2022)
Fulvifomes costaricensis	JV 1407/87	Costa Rica	MH390412	MH390387	Wu et al. (2022)
Fulvifomes costaricensis	JV 1408/14	Costa Rica	MH390413	MH390385	Wu et al. (2022)
Fulvifomes costaricensis	JV 1607/103	Costa Rica	MH390414	MH390386	Wu et al. (2022)
Fulvifomes dracaenicola	Dai 22097	China	MW559800	MW559805	Wu et al. (2022)
Fulvifomes dracaenicola	Dai 22093	China	MW559799	MW559804	Wu et al. (2022)
Fulvifomes elaeodendri	CMW 47808	South Africa	MH599093	MH599131	Wu et al. (2022)
Fulvifomes elaeodendri	CMW 47825	South Africa	MH599094	MH599134	Wu et al. (2022)
Fulvifomes elaeodendri	CMW 47909	South Africa	MH599096	MH599132	Wu et al. (2022)
Fulvifomes elaeodendri	CMW 48154	South Africa	MH599097	MH599135	Wu et al. (2022)
Fulvifomes elaeodendri	CMW 48610	South Africa	MH599095	MH599133	Wu et al. (2022)
Fulvifomes fastuosus	LWZ 20140731-13	Thailand	KR905674	KR905668	Zhou (2015)
Fulvifomes fastuosus	LWZ 20140718-29	Thailand	KR905673	–	Zhou (2015)
Fulvifomes fastuosus	Dai 18292	Vietnam	MH390411	MH390381	Wu et al. (2022)
Fulvifomes floridanus	JV 0904/65	USA	MH390422	–	Wu et al. (2022)
Fulvifomes floridanus	JV 0312/23.1	USA	MH390423	–	Wu et al. (2022)
Fulvifomes floridanus	JV 0904/76	USA	MH390424	MH390388	Wu et al. (2022)
Fulvifomes fragilis	**JV 2402/50-J-1**	**Ecuador**	**PV368085**	**PV368092**	**Present study**
Fulvifomes fragilis	**JV 2402/50-J-2**	**Ecuador**	**PV368086**	–	**Present study**
Fulvifomes grenadensis	JV 1212/2J	USA	KX960756	–	Ji et al. (2017)
Fulvifomes grenadensis	1607/66	Costa Rica	KX960758	–	Ji et al. (2017)
Fulvifomes hainanensis	Dai 11573	China	KC879263	JX866779	Zhou (2014)
Fulvifomes halophilus	XG 4	Thailand	JX104705	JX104752	Wu et al. (2022)
Fulvifomes halophilus	JV 1502/4	USA	MH390427	MH390392	Wu et al. (2022)
Fulvifomes imazekii	FFPRI 421006	Japan	LC315787	LC315778	Hattori et al. (2022)
Fulvifomes imazekii	FFPRI 421007	Japan	LC315788	LC315779	Hattori et al. (2022)
Fulvifomes imbricatus	LWZ 20140728-16	Thailand	KR905677	KR905670	Zhou (2015)
Fulvifomes imbricatus	LWZ 20140729-25	Thailand	KR905678	–	Zhou (2015)
Fulvifomes imbricatus	LWZ 20140729-26	Thailand	KR905679	KR905671	Zhou (2015)
Fulvifomes indicus	Yuan 5932	China	KC879261	JX866777	Zhou (2014)
Fulvifomes indicus	O 25034	Zimbabwe	KC879262	KC879259	Wu et al. (2022)
Fulvifomes jawadhuvensis	SKM-JMR5	India	MW040079	MW048886	GenBank
Fulvifomes jouzaii	JV 1504/16	Costa Rica	MH390425	MH390400	Wu et al. (2022)
Fulvifomes jouzaii	JV 1504/39	Costa Rica	MH390426	–	Wu et al. (2022)
Fulvifomes kawakamii	PPT152	Brazil	MH048095	MH048085	Zhou (2015)
Fulvifomes kawakamii	CBS 428.86	USA	–	AY059028	Wagner and Fischer (2002)
Fulvifomes labyrinthus	SFC20160126-30	FS Micronesia	OR168711	–	Suh et al. (2024)
Fulvifomes labyrinthus	SFC20160126-34	FS Micronesia	OR168712	–	Suh et al. (2024)
Fulvifomes lloydii	Dai 10809	China	MH390428	MH390378	Wu et al. (2022)

Species name	Sample no.	Location	GenBank accessions no.		References
			ITS	nLSU	
Fulvifomes lloydii	Dai 9642	China	MH390429	MH390379	Wu et al. (2022)
Fulvifomes lloydii	Dai 11978	China	MH390430	MH390380	Wu et al. (2022)
Fulvifomes luteoumbrinus	CBS 296.56	USA	AY558603	AY059051	Wagner and Fischer (2002)
Fulvifomes mangroviensis	KSM-MP1	Tamil Nadu	MW040083	MW048909	Tan et al. (2022)
Fulvifomes mangroviensis	KSM-MP12a	Tamil Nadu	OM987221	OM897222	Tan et al. (2022)
Fulvifomes merrillii	6Kout	Thailand	MH390416	MH390383	Wu et al. (2022)
Fulvifomes merrillii	Dai 12094	China	MH390415	MH390376	Wu et al. (2022)
Fulvifomes nakasoneae	JV 1109/62	USA	MH390407	MH390376	Wu et al. (2022)
Fulvifomes nakasoneae	JV 0904/68	USA	MH390408	MH390373	Wu et al. (2022)
Fulvifomes nakasoneae	JV 1109/77	USA	MH390409	MH390374	Wu et al. (2022)
Fulvifomes nakasoneae	JV 0312/22.11	USA	MH390410	MH390375	Wu et al. (2022)
Fulvifomes nilgheriensis	CBS 209.36	USA	AY558633	AY059023	Wagner and Fischer (2002)
Fulvifomes nilgheriensis	URM 3028	Brazil	MH390431	MH390384	Wu et al. (2022)
Fulvifomes nonggangensis	GXU1127	China	MT571504	MT571502	Zheng et al. (2021)
Fulvifomes nonggangensis	GXU2254	China	MT571503	MT571501	Zheng et al. (2021)
Fulvifomes rhizophorus	SFC20170118-26	FS Micronesia	OR168715	OR168723	Suh et al. (2024)
Fulvifomes rhizophorus	SFC20170120-06	FS Micronesia	OR168713	OR168724	Suh et al. (2024)
Fulvifomes rhizophorus	SFC20170120-09	FS Micronesia	OR168714	OR168725	Suh et al. (2024)
Fulvifomes rhytiphloeus	JV 1704/71	Costa Rica	MZ506738	MZ505207	Wu et al. (2022)
Fulvifomes rhytiphloeus	JV 1808/76	French Guiana	MZ506739	MZ505208	Wu et al. (2022)
Fulvifomes rigidus	Dai 17496	China	MH390432	MH390398	Wu et al. (2022)
Fulvifomes rigidus	Dai 17507	China	MH390433	MH390399	Wu et al. (2022)
Fulvifomes rimosus	M 2392655	Australia	MH628255	MH628017	Wu et al. (2022)
Fulvifomes robiniae	CBS 211.36	USA	AY558646	AF411825	GenBank
Fulvifomes robiniae	—	—	EF088656	—	Wagner and Fischer (2002)
Fulvifomes siamensis	XG 2	Thailand	JX104709	JX104756	Zhou (2014)
Fulvifomes siamensis	Dai 18309	Vietnam	MH390434	MH390389	Wu et al. (2022)
Fulvifomes sp.	JV 2402/43-J	Ecuador	PV368087	PV368093	Present study
Fulvifomes squamosus	CS385	Peru	MF479268	MF479265	Salvador-Montoya et al. (2018)
Fulvifomes squamosus	CS444	Peru	MF479269	MF479264	Salvador-Montoya et al. (2018)
Fulvifomes subindicus	Dai 17743	China	MH390435	MH390393	Wu et al. (2022)
Fulvifomes subindicus	Cui 13908	China	MH390436	MH390394	Wu et al. (2022)
Fulvifomes submerrillii	Dai 17911	China	MH390405	MH390371	Wu et al. (2022)
Fulvifomes submerrillii	Dai 17917	China	MH390406	MH390372	Wu et al. (2022)
Fulvifomes thailandicus	LWZ 20140731-1	Thailand	KR905672	KR905665	Zhou (2015)
Fulvifomes thiruvannamalaiensis	MUBL 4013	India	NR_185632	NG_228882	GenBank
Fulvifomes thiruvannamalaiensis	SKM-JMR11	India	MZ221598	MZ221600	GenBank
Fulvifomes tubogeneratus	GXU2468	China	MT580805	MT580800	Zheng et al. (2021)
Fulvifomes tubogeneratus	GXU2478	China	MT580806	MT580801	Zheng et al. (2021)
Fulvifomes wrightii	CTES:568251	Argentina	OQ807192	OQ924560	Martínez et al. (2023)
Fulvifomes wrightii	CTES:568252	Argentina	OQ807191	OQ924561	Martínez et al. (2023)
Fulvifomes wrightii	CTES:568253	Argentina	OQ807194	OQ924558	Martínez et al. (2023)
Fulvifomes xylocarpicola	MU 8	Thailand	JX104676	JX104723	Zhou (2014)
Inocutis tamaricis	CBS 384.72	Turkmenistan	AY558604	MH872221	Vu et al. (2019)
Inonotus hispidus	S45	Spain	EU282482	EU282484	GenBank
Phellinus betulinus	CBS 122.40	USA	MH856059	MH867554	Wu et al. (2022)
Phellinus populicola	CBS 638.75	Finland	MH860960	MH872729	Wu et al. (2022)

Bold = new taxa, — refers the data unavailability.

Results

Molecular phylogeny

In this study, 101 fungal samples representing 51 taxa of *Fulvifomes* were included in the phylogenetic analyses, and two samples of the genus *Phellinus* were used as outgroups. The phylogenetic trees were constructed using a total

of 2,061 base pairs (bp) of alignments, including 1,151 bp of ITS and 910 bp of nLSU. The best-fit model applied in the Bayesian analysis was GTR+I+G, lset nst = 6, rates = invgamma, and prset statefreqpr = dirichlet (1, 1, 1, 1). Bayesian analysis resulted in an average standard deviation of split frequencies of 0.009917. The topologies of the generated ML and BI trees are nearly congruent. Thus, only the topologies inferred from the ML method were presented, along with bootstrap values (≥ 50%) from the ML method and BPPs (≥ 0.9) from the BI method. In the phylogeny of *Fulvifomes* (Fig. 1), the two new species each formed an independent lineage with strong support: *Fulvifomes bolivianus* (BS = 98% in ML, BPP = 1.00) and *Fulvifomes fragilis* (BS = 100% in ML, BPP = 1.00).

The ITS sequences showed significant alignments in the NCBI database (https://blast.ncbi.nlm.nih.gov/Blast.cgi) for *Fulvifomes bolivianus*, with all of the top ten sequences having less than 95% similarity, the highest being *F. squamosus* (CS385) at 94.8%. As for *Fulvifomes fragilis*, the similarities of the top ten ITS sequences were less than 90%, and they represent multiple species in *Fulvifomes*. The alignment results in the NCBI database are consistent with our phylogeny (Fig. 1).

Taxonomy

Fulvifomes bolivianus **Jian Chen, Yuan Yuan, K.Y. Luo, Y.C. Dai & Vlasák, sp. nov.**
MycoBank No: 858480
Figs 2, 3

Diagnosis. *Fulvifomes bolivianus* is related to *F. squamosus* Salvador-Montoya & Drechsler-Santos, but *F. squamosus* differs from *F. bolivianus* by applanate to triquetrous pilei, a monomitic hyphal system in context, and larger pores (5–6 per mm vs. 7–8 per mm).

Holotype. Bolivia. • St. Cruz Dept., Refugio los Volcanes, altitude 1100 m, dead angiosperm tree, 1.XI.2023, leg J. Vlasák Jr., JV 2311/6-J (BJFC 044745).

Etymology. *Bolivianus* (Lat.): refers to the type of species being found in Bolivia.

Description. Basidiomata perennial, pileate, solitary, without distinctive odor or taste, and woody hard when fresh, light in weight when dry. Pilei ungulate, projecting up to 11 cm and 5 cm wide and 2.5 cm thick at base. Pileal surface olivaceous when dry, encrusted, rough, concentrically sulcate, irregularly cracked; pileal margin brown, obtuse. Pore surface umber, with a reddish tint, unglancing; sterile margin distinct, fulvous, up to 3 mm wide; pores circular, 7–8 per mm; dissepiments thick, entire. Context umber, woody hard, zonate, up to 5 mm thick. Tubes fulvous, woody hard, up to 1 mm long, tube layers indistinctly stratified.

Hyphal structure. Hyphal system dimitic in trama and context; generative hyphae simple septate; tissue becoming blackish brown in KOH.

Context. Generative hyphae hyaline to brown, thick-walled, unbranched, simple septate, 2–2.5 µm in diameter; skeletal hyphae dominant, golden yellow to brown, thick-walled, unbranched, aseptate, more or less straight, regularly arranged, 4–6.5 µm in diameter.

Tubes. Generative hyphae hyaline to brown, thick-walled, unbranched, simple septate, 2–3 µm in diameter; skeletal hyphae frequent, golden yellow to brown, thick-walled with a narrow lumen, unbranched, aseptate, more or less straight, subparallel along tubes, 2.5–4 µm in diameter. Setae or setal hyphae absent;

Figure 1. Maximum likelihood tree illustrating the phylogeny of *Fulvifomes* based on the combined dataset of ITS + nLSU sequences. The maximum likelihood bootstrap values (≥50) and Bayesian posterior probability values (≥0.90) are indicated above the branches. The new species is in bold.

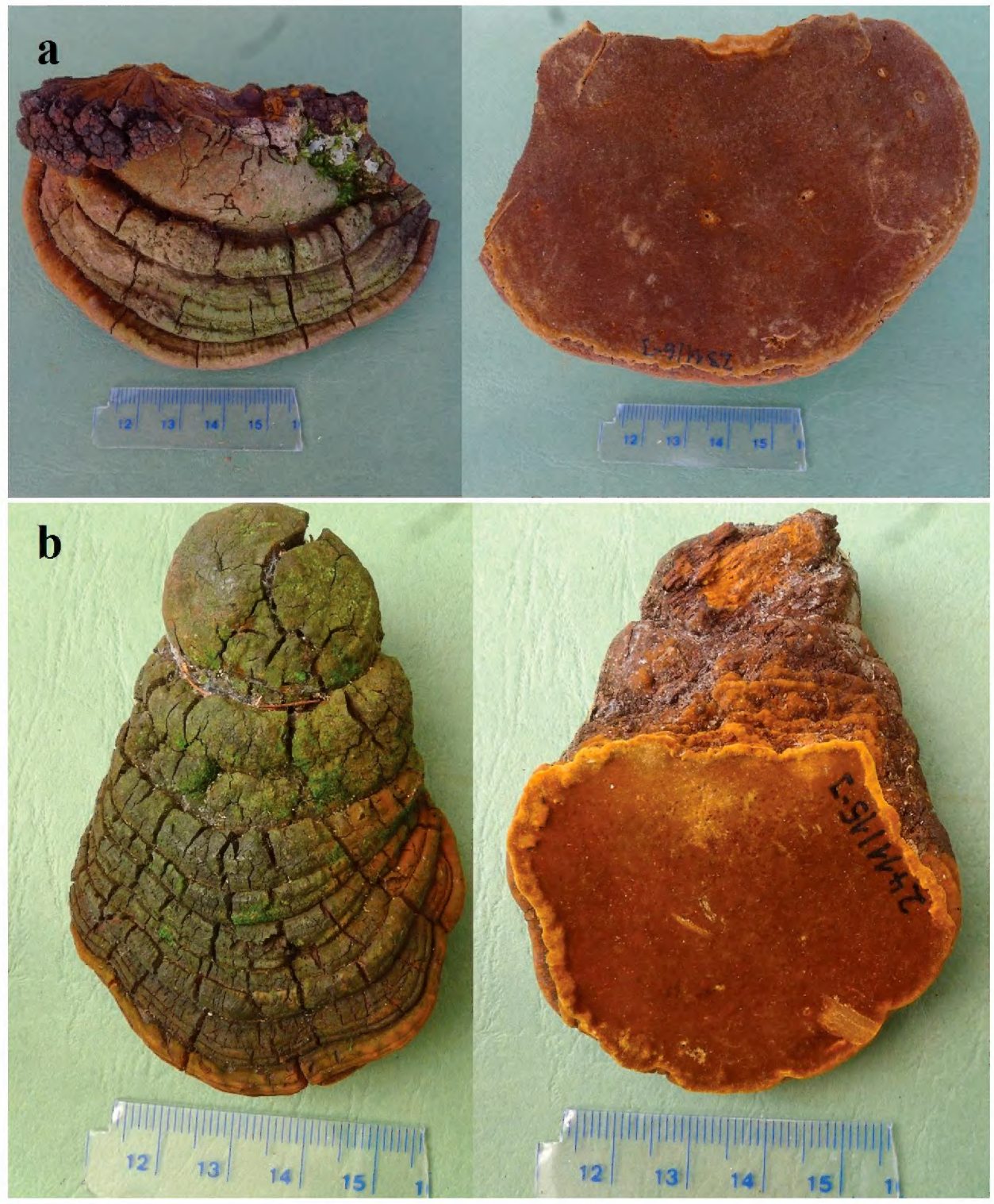


Figure 2. Basidiomata of *Fulvifomes bolivianus* (**a.** Holotype, JV 2311/6-J; **b.** Paratype JV 2411/15J).

cystidioles thin-walled, hyaline, varies in shape, fusoid to ventricose with elongated apical portion, 8.5–18 × 3.5–5.5 µm; basidia clavate to barrel-shaped, with four sterigmata and a simple basal septum, 15–18 × 6–7 µm; basidioles in shape similar to basidia, slightly smaller than basidia.

Basidiospores subglobose, yellowish brown, thick-walled, smooth, IKI–, CB–, (4.4–)4.7–5.4(–5.7) × (3.5–)4–5(–5.3) µm, L = 5.04 µm, W = 4.50 µm, Q = 1.12 (n = 30/1).

Type of rot. White rot.

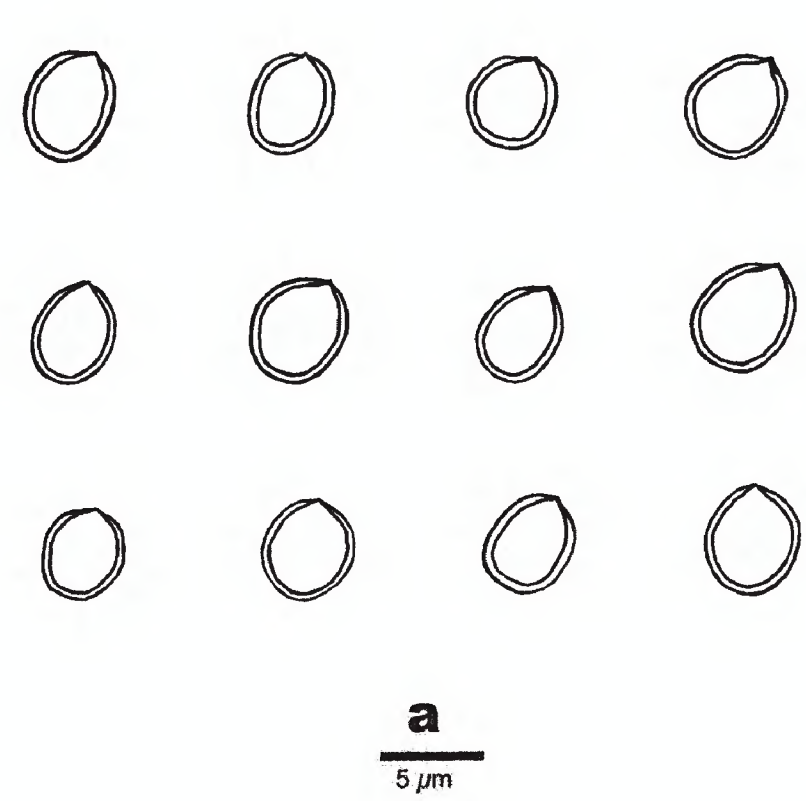
Additional specimen examined (paratype). Bolivia. • St. Cruz Dept., Refugio los Volcanes, altitude 1100 M, dead angiosperm tree, 1.XI.2024, leg J. Vlasák Jr., JV 2411/15J.

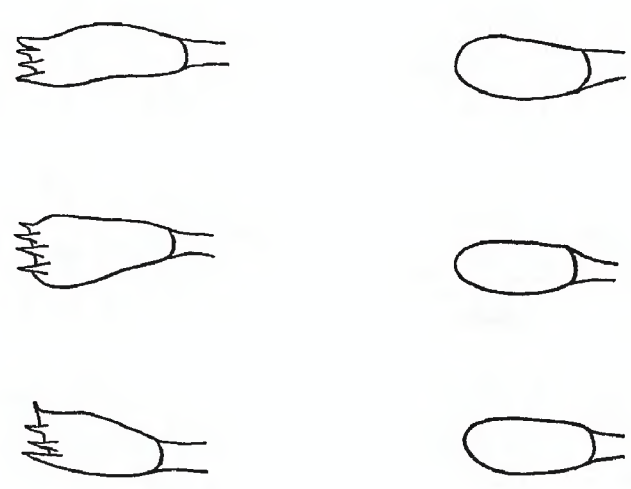
***Fulvifomes fragilis* Jian Chen, Yuan Yuan, K.Y. Luo, Y.C. Dai & Vlasák, sp. nov.**

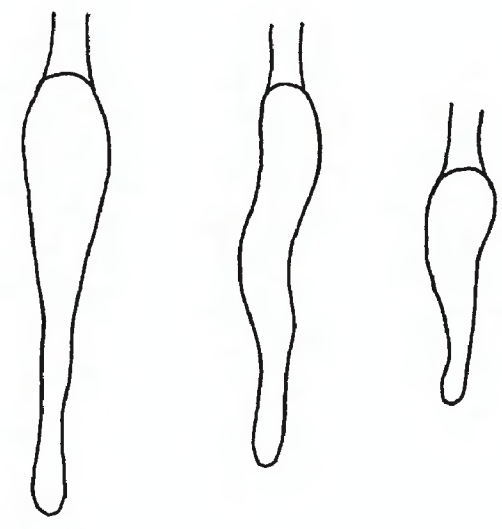
MycoBank No: 858481

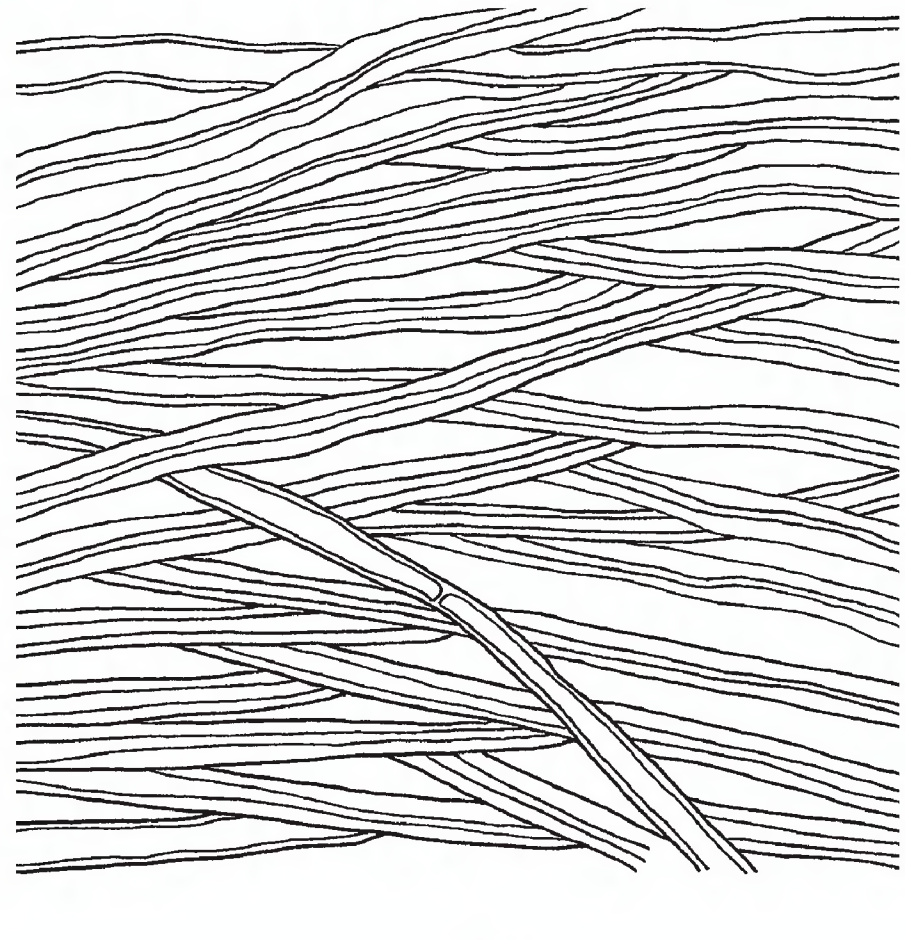
Figs 4, 5

Diagnosis. *Fulvifomes fragilis* is related to *F. luteoumbrinus* (Romell) Y.C. Dai & Vlasák, but *F. luteoumbrinus* differs from *F. fragilis* by a monomitic hyphal system and larger basidiospores (5.0–6.0 × 4.0–5.5 µm vs. 3.9–5.1 × 3–3.7 µm).









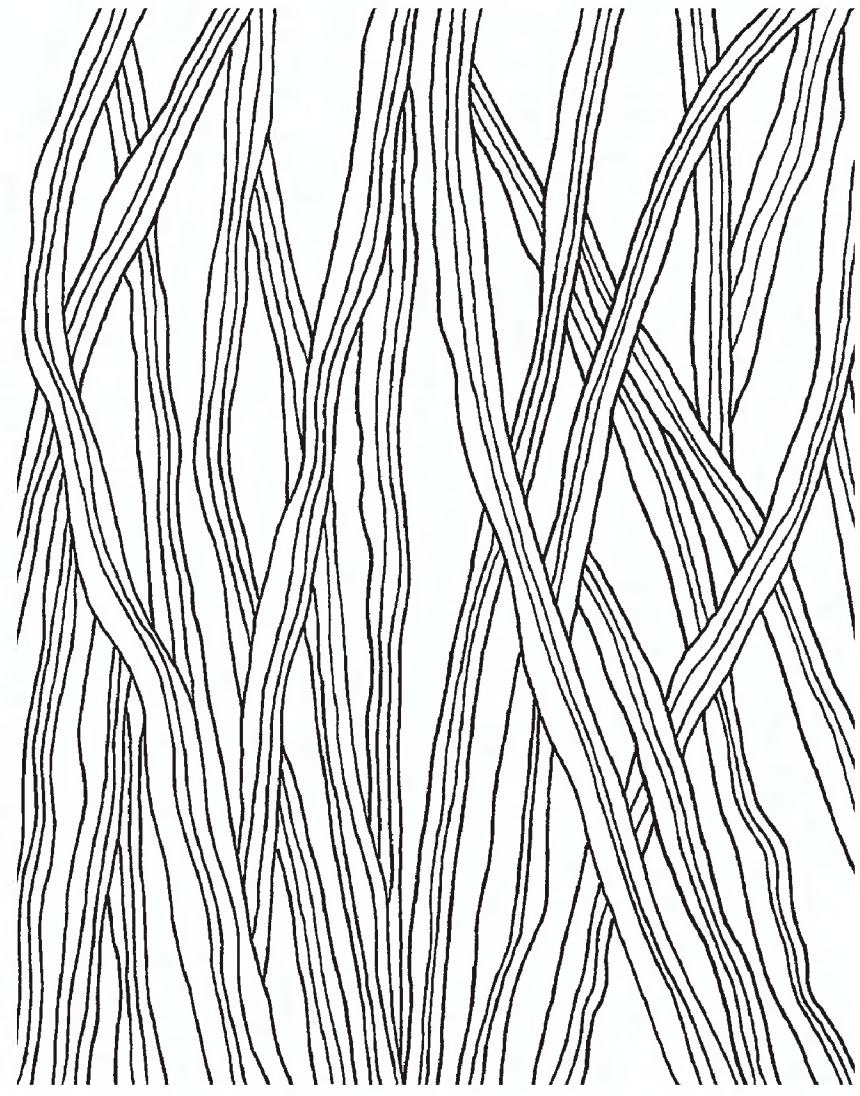


Figure 3. Microscopic structures of *Fulvifomes bolivianus* (Holotype, JV 2311/6-J). **a.** Basidiospores; **b.** Basidia and basidioles; **c.** Cystidioles; **d.** Hyphae from context; **e.** Hyphae from tube trama.

Holotype. Ecuador. • Macará, Reserva Jorupe, dry tropical forest, altitude 650 m, on roots of rotten angiosperm tree, 21.II.2024, leg J. Vlasák Jr., JV 2402/50-J-1 (BJFC 053708-1).

Figure 4. Basidiomata of *Fulvifomes fragilis* (Holotype, JV 2402/50J-1). Scale bar: 1 cm.

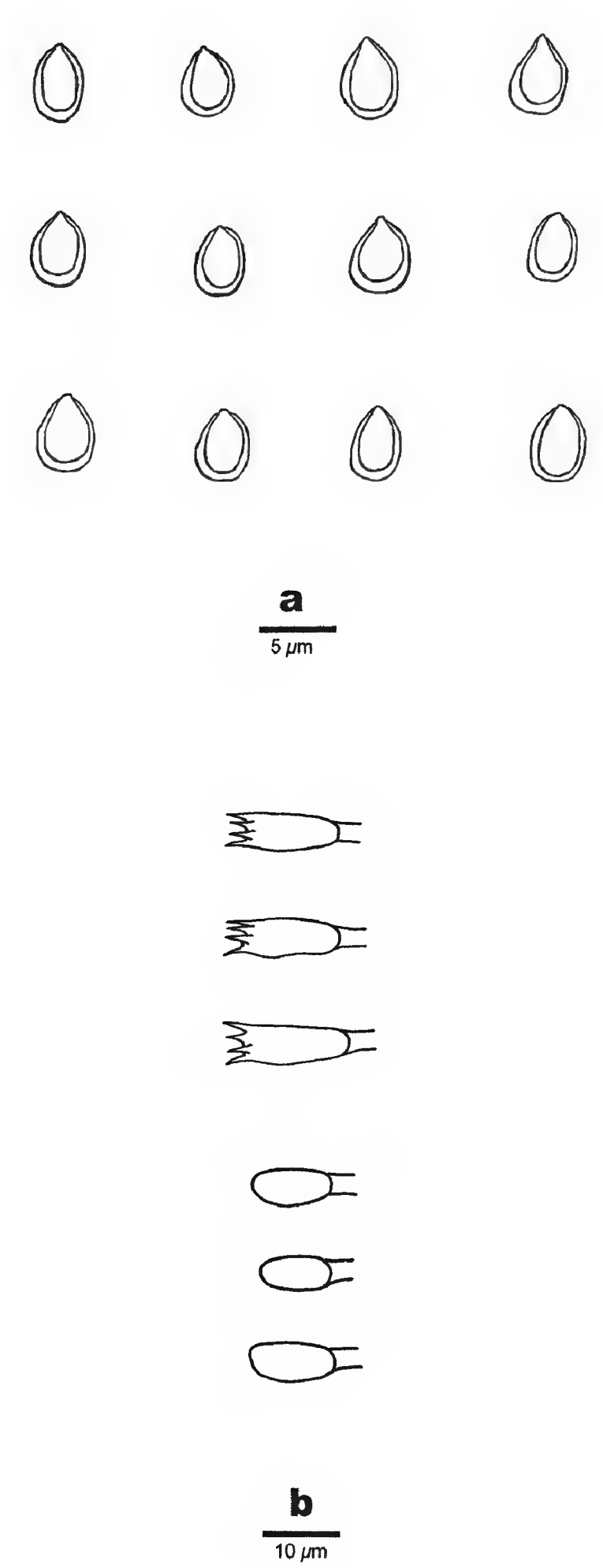
Etymology. *Fragilis* (Lat.): refers to the species having brittle basidiomata when dry.

Description. Basidiomata annual, pileate, imbricate, without distinctive odor or taste, and woody hard to brickle when dry. Pilei sessile, projecting up to 7 cm and 11 cm wide and 8 mm thick at base. Pileal surface curry yellow to yellowish brown when dry, rough; pileal margin yellowish brown, narrow. Pore surface yellow, rugged; sterile margin distinct, yellow, up to 4 mm wide; pores circular to elliptical, 5–6 per mm; dissepiments thick, entire. Context lemon yellow, woody hard, up to 6 mm thick. Tubes concolorous with context, woody hard, up to 0.5 mm long.

Hyphal structure. Hyphal system dimitic in trama and context; generative hyphae simple septate; tissue becoming blackish brown in KOH.

Context. Generative hyphae pale yellow, thick-walled, occasionally branched, frequently simple septate, 3–4 µm in diameter; skeletal hyphae dominant, yellowish to golden yellow, thick-walled, unbranched, aseptate, more or less straight, regularly arranged, 3–4 µm in diameter.

Tubes. Generative hyphae pale yellow, thick-walled, rarely branched, frequently simple septate, 2.5–4.5 µm in diameter; skeletal hyphae frequent, yellowish to golden yellow, thick-walled with a narrow to wide lumen, unbranched, aseptate, more or less straight, subparallel along tubes, 2.5–4.5 µm in diameter. Setae or setal hyphae absent; cystidioles absent; basidia clavate to barrel-shaped, with four sterigmata and a simple basal septum, 11–14 × 5–6 µm; basidioles in shape similar to basidia, slightly smaller than basidia.



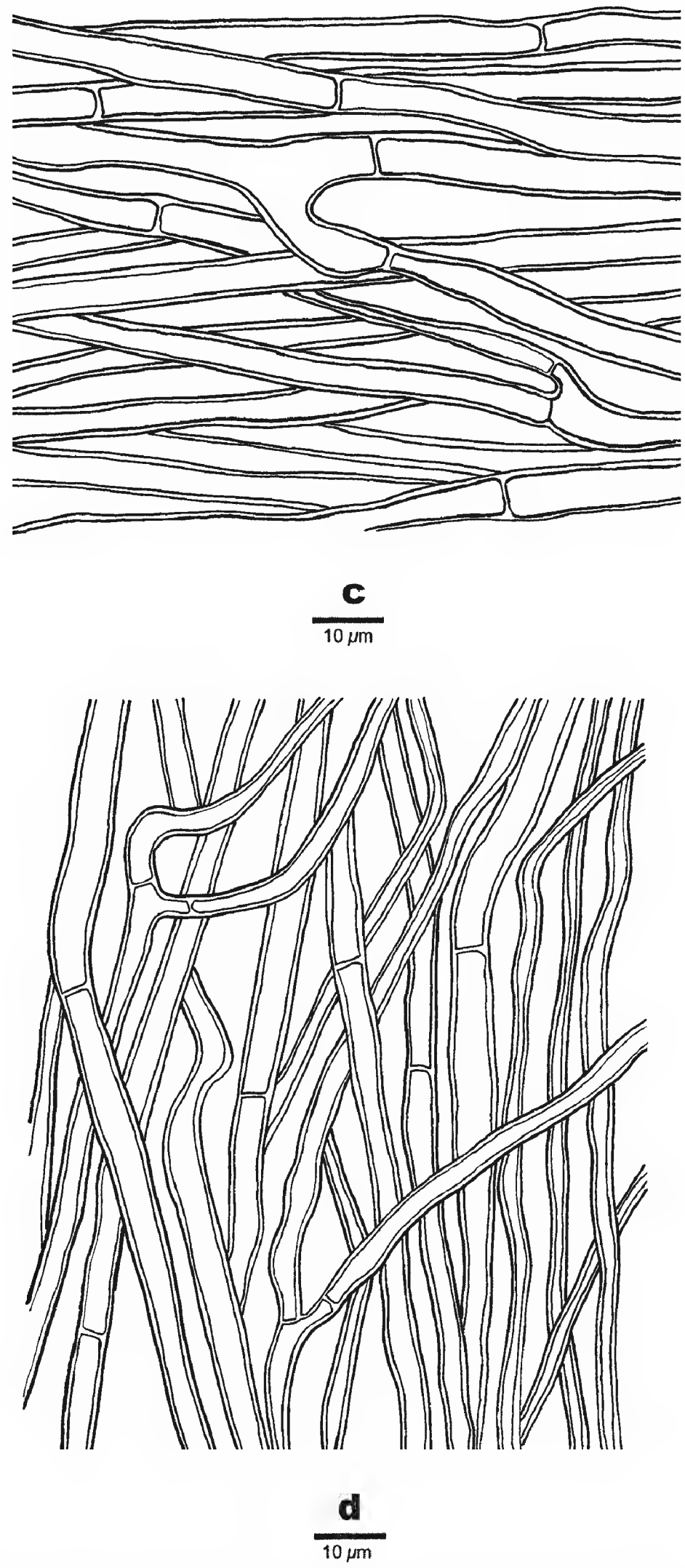


Figure 5. Microscopic structures of *Fulvifomes fragilis* (holotype, JV 2402/50-J-1). **a.** Basidiospores; **b.** Basidia and basidioles; **c.** Hyphae from context; **d.** Hyphae from tube trama.

Basidiospores broadly ellipsoid, yellowish brown, thick-walled, smooth, some collapsed, IKI–, CB–, 3.9–5.1 × (2.9–)3–3.7(–3.8) µm, L = 4.38 µm, W = 3.38 µm, Q = 1.30–1.32 (n = 60/2).

Type of rot. White rot.

Additional specimen examined (paratype). Ecuador. • Macará, Reserva Jorupe, dry tropical forest, altitude 650 m, on roots of rotten angiosperm tree, 21.II.2024, leg J. Vlasák Jr., JV 2402/50-J-2 (BJFC 053708-2).

Discussion

Most *Fulvifomes* species have relatively uniform basidiospores and lack setae, making morphological determination problematic (Dai 2010; Wu et al. 2022). DNA-based phylogenetics, however, provides a powerful tool that enables the discrimination of closely related species. Based on both phylogenetic analyses and morphology, we have described *Fulvifomes fragilis* and *Fulvifomes bolivianus* as new to science in this study. They fit well in *Fulvifomes*, with annual to perennial, pileate basidiocarps, broadly ellipsoid basidiospores, and the absence of setae or setal hyphae. Phylogenetically, they formed distinct lineages within the *Fulvifomes* clade based on ITS + nLSU datasets (Fig. 1).

Morphologically, *Fulvifomes bolivianus* is most similar to *F. krugiodendri* Y.C. Dai, X.H. Ji & Vlasák by sharing perennial and pileate basidiocarps, ungulate and cracked pilei, a dimitic hyphal system, and thick, entire dissepiments. Moreover, they have approximately the same size pores and basidiospores. *F. krugiodendri* differs from *F. bolivianus* by its dark gray pileal surface, grayish brown, glossy pore surface, and its distribution in Florida, USA (Ji et al. 2017). Phylogenetically, *F. bolivianus* is related to *F. squamosus* Salvador-Montoya & Drechsler-Santos, but *F. squamosus* is different from *F. bolivianus* by applanate to triquetrous pilei, a monomitic hyphal system in context, and larger pores (5–6 per mm vs. 7–8 per mm) (Salvador-Montoya et al. 2018).

Fulvifomes fragilis is phylogenetically related to *F. luteoumbrinus* (Romell) Y.C. Dai & Vlasák (= *Inocutis porrecta* (Murrill) Baltazar), a somewhat aberrant species within *Fulvifomes* for which, at one time, the genus *Aurificaria* (Romell) D.A. Reid was established due to its trametoid basidioma and very dark spores. Phylogenetic analysis revealed, however, a close relationship with *Fulvifomes* species, and it was accepted as *Fulvifomes* with a unique combination of features occurring in different species of *Fulvifomes* (Wu et al. 2022). *F. luteoumbrinus* differs from *F. fragilis* by a monomitic hyphal system and larger basidiospores (5–6 × 4–5.5 µm vs. 3.9–5.1 × 3–3.7 µm) (Baltazar et al. 2010; Sakayaroj et al. 2012). Morphologically, *Fulvifomes fragilis* resembles *F. indicus* (Massee) L.W. Zhou by sharing annual, pileate basidiocarps, approximately the same size pores, and the absence of setae or setal hyphae, but *F. indicus* has a monomitic hyphal system, larger basidiospores (5.4–6.5 × 4.7–5.5 µm vs. 3.9–5.1 × 3–3.7 µm), and a distribution in Southeast Asia and Australia (Zhou 2014). In addition, although *F. fragilis* shares a bright yellow color changing red with KOH and thin, flabelliform, often semistipitate fruitbodies with *Flaviporellus splitgerberi* (Mont.) Murrill (≡ *Inonotus splitgerberi* (Mont.) Ryvarden) (Wu et al. 2022), it forms a distinct clade within the *Fulvifomes* phylogeny.

In the phylogeny of Hymenochaetaceae, *Fulvifomes* is related to *Flaviporellus* and *Phylloporia*, and the three genera share the absence of setae and thick-colored basidiospores. However, *Flaviporellus* has basidiocarps becoming vivid deep red in KOH and collapsing basidiospores when mature, while *Phylloporia* grows almost always parasitically on living plants and has a duplex context. *Fulvifomes* usually grows on dead angiosperm trees or wood, has basidiocarps with homogeneous context that turn blackish brown in KOH, and its mature basidiospores are mostly not collapsed (Wu et al. 2022). In addition, most *Fulvifomes* species occur in tropical or subtropical areas (Wu et al. 2022); only *F. rimosus* (Berk.)

Fiasson & Niemelä has been recorded in Europe (Ryvarden and Melo 2014). The two new species of *Fulvifomes* from South America discovered in this study also grow on dead angiosperm trees (*F. bolivianus*) or rotten wood (*F. fragilis*), and *F. fragilis* has collapsed basidiospores that become yellowish brown in KOH.

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Additional information

Conflict of interest

The authors have declared that no competing interests exist.

Ethical statement

No ethical statement was reported.

Use of AI

No use of AI was reported.

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Author contributions

All authors designed the research, contributed to data analysis and interpretation, prepared the samples, and drafted the manuscript.

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Data availability

All of the data that support the findings of this study are available in the main text.

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